AMENDMENTS TO THE CLAIMS

The following listing of claims will replace all prior versions, and listings, of claims in the application.

Claim 1 (currently amended): A method of ~~designing~~ identifying a compound ~~able to bind to a molecule of the insulin receptor family and to modulate an activity mediated by the molecule, including the step of assessing the stereochemical complementarity between the compound and the receptor site of the molecule wherein the receptor site includes~~ which modulates binding of a natural ligand to the insulin receptor (IR), IGF-1 receptor (IGF-1R) or insulin receptor related receptor (IRR) or which modulates signal transduction via IR, IGF-1R or IRR, which method comprises:

(A) assessing the stereochemical complementarity between the compound and a molecule, wherein the molecule comprises

(i[[a]]) amino acids 1 to 462 of ~~the receptor for~~ [[IGF-1]] IGF-1R, having the atomic coordinates substantially as shown in Figure 1;

(ii [[b]]) a subset of said amino acids, or;

(iii [[c]]) amino acids present in the amino acid sequence of ~~a member of the insulin receptor family~~ IR or IRR, ~~which~~ that form an equivalent three-dimensional structure to that of the ~~receptor~~ molecule as depicted in Figure 1;

(B) obtaining a compound that possesses stereochemical complementarity to the molecule; and

(C) testing the compound for its ability to

(i) modulate binding of a natural ligand to IR, IGF-1R or IRR; or

(ii) modulate signal transduction via IR, IGF-1R or IRR.

Claims 2-20 (canceled).

Claim 21 (currently amended): A computer-assisted method for identifying ~~potential compounds~~ a compound able to bind to ~~a molecule of the insulin receptor family and to modulate an activity mediated by the molecule~~ IR, IGF-1R or IRR, using a programmed computer including a processor, an input device, and an output device, including the steps of:

(a)   inputting into the programmed computer, through the input device, data comprising the atomic coordinates of the IGF-1R molecule as shown in Figure 1, or a subset thereof;

(b)   generating, using computer methods, a set of atomic coordinates of a structure that possesses stereochemical complementarity to the atomic coordinates of the IGF-1R ~~site~~ molecule as shown in Figure 1, or a subset thereof, thereby generating a criteria data set;

(c)   comparing, using the processor, the criteria data set to a computer database of chemical structures;

(d)   selecting from the database, using computer methods, chemical structures which are structurally similar to a portion of said criteria data set; and

(e)   outputting, to the output device, the selected chemical structures which are similar to a portion of the criteria data set.

Claim 22 (canceled).

Claim 23 (currently amended): A computer-assisted method according to claim 21, which further includes the step of ~~selecting one or more~~ obtaining a compound with a chemical ~~structures from steps~~ structure selected in steps (d) and (e), and testing the compound for the ability to ~~which interact with the receptor site of the molecule in a manner which prevents the~~ prevent binding of a natural ~~ligands to the receptor site~~ ligand to IR, IGF-1R or IRR.

Claim 24 (currently amended): A computer-assisted method according to claim 21, which further includes the step of obtaining a compound with a chemical structure selected in steps (d) and (e), and testing the compound for the ability to decrease ~~an activity mediated by the receptor~~ signal transduction via IR, IGF-1R or IRR.

Claim 25 (canceled).

Claim 26 (currently amended): A computer-assisted method to claim [[25]] 21, ~~further including~~ which further includes the step of obtaining a ~~molecule~~ compound with a chemical structure selected in steps (d) and (e), and testing the compound for the ability to increase ~~an activity mediated by the receptor~~ signal transduction via IR, IGF-1R or IRR.

Claims 27-29 (canceled).

Claim 30 (currently amended): A The method according to claim [[29]] 1, in which the ~~test~~ testing in step (C) is carried out *in vitro*.

Claim 31 (currently amended): A The method according to claim [[29]] 30, in which the test is a high throughput assay.

Claim 32 (currently amended): A The method according to claim [[29]] 1, in which the ~~test~~ testing in step (C) is carried out *in vivo*.

Claim 33 (canceled).

Claim 34 (new): The method of claim 1, wherein step (C)(ii) involves testing the compound for the ability to modulate IR, IGF-1R or IRR mediated cell proliferation.

Claim 35 (new): The method of claim 1, wherein the one or more subsets of amino acids in step (A)(ii) is defined by amino acids 191-290 of IGF-1R positioned at atomic coordinates substantially as shown in Figure 1.

Claim 36 (new): The method of claim 1, wherein the amino acids in step (A) (iii) are present in the amino acid sequence of IR or IRR and form an equivalent three-dimensional structure

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to that of the region defined by amino acids 191-290 of IGF-1R positioned at atomic coordinates substantially as shown in Figure 1.

Claim 37 (new): The method of claim 1, wherein the one or more subsets of amino acids in step (A)(ii) is defined by amino acids 223-274 of IGF-1R positioned at atomic coordinates substantially as shown in Figure 1.

Claim 38 (new): The method of claim 1, wherein the amino acids in step (A) (iii) are present in the amino acid sequence of IR or IRR and form an equivalent three-dimensional structure to that of the region defined by amino acids 223-274 of IGF-1R positioned at atomic coordinates substantially as shown in Figure 1.

Claim 39 (new): The method of claim 1 which further includes the step of modifying the compound such that the compound comprises structural regions able to make contact with amino acid residues at the surface of the molecule as depicted in Figure 2.

Claim 40 (new): The method of claim 1 which further includes the step of modifying the compound such that the compound comprises structural regions able to make contact with amino acid residues in the region of the interface between the L1 domain and the cys-rich domain as depicted in Figure 2.

Claim 41 (new): The method of claim 1, wherein one or more subsets of amino acids in step (A)(ii) are the amino acids that form the β-sheet of the L1 domain of IGF-1R.

Claim 42 (new): The method of claim 1, wherein one or more subsets of amino acids in step (A)(iii) are present in the amino acid sequence of IR or IRR and form an equivalent three dimensional structure to that of the β-sheet of the L1 domain of IGF-1R.

Claim 43 (new): The method of claim 1 in which the compound is identified from test compounds in a database.

Claim 44 (new): The method of claim 1, which further includes the step of selecting a compound that increases signal transduction via IR, IGF-1R or IRR.

Claim 45 (new): The method of claim 1, which further includes the step of selecting a compound that decreases signal transduction via IR, IGF-1R or IRR.

Claim 46 (new): The method of claim 1, which further includes the step of selecting a compound that inhibits or prevents the binding of a natural ligand to IR, IGF-1R or IRR.

Claim 47 (new): A method of identifying a compound that binds to IR, IGF-1R or IRR, the method comprising:

(A)   assessing the stereochemical complementarity between the compound and a molecule, wherein the molecule comprises

(i)   amino acids 1 to 462 of IGF-1R, having the atomic coordinates substantially as shown in Figure 1;

(ii)   a subset of said amino acids, or;

(iii)   amino acids present in the amino acid sequence of IR or IRR that form an equivalent three-dimensional structure to that of the molecule as depicted in Figure 1;

(B)   obtaining a compound that possesses stereochemical complementarity to the molecule; and

(C)   selecting a compound that has a K_b or K_I of less than 10^{-6} M for IR, IGF-1R or IRR.

Claim 48 (new): The method according to claim 47 wherein the K_b is less than 10^{-8} M.

Claim 49 (new): The method according to claim 47 wherein the K_I is less than 10^{-8} M.